

SEQUENCE LISTING

<110> Kihara Memorial Yokohama Foundation for the Advancement of Life Sciences
City of Yokohama

<120> TRF2 DNA-binding domain mutant proteins, telomeric DNA mutants, and use of a structure of a complex between a TRF2 DNA binding domain and a double-stranded DNA molecule

<130> FP-047PCT

<140> 10/590,464
<141> 2006-08-23

<150> JP P2004-046238

<151> 2004-02-23

<160> 29

<170> PatentIn version 3.1

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<212> DNA

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gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac 96
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
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tgg gct gcc att tct aaa aat tac cca ttt gtt aac cga aca gct gtg      144
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atg att aag gat cgc tgg cgg acc atg aaa aga ctt ggc atg aac 189
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Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
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Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ala Val
35 40 45

Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn
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gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac 96
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
20 25 30

tgg gct gcc att tct aaa aat tac cca ttt gtt aac cga aca gct gtg
Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ala Val 144
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35 40 45

Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn
50 55 60

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<223> Mutant A471S of hTRF2-DBD

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gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac 96
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
20 25 30

tgg tct gcc att tct aaa aat tac cca ttt gtt aac cga aca gct gtg 144
Trp Ser Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ala Val
35 40 45

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gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac 96
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
20 25 30

tgg gct gcc att tct aaa aat tac cca ttt gtt aac cga aca tct gtg 144
Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ser Val
35 40 45

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gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac 96
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
20 25 30

tgg gct gcc att tct aaa aat tac cca ttt gtt aac cga aca gct gtg 144
Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ala Val
35 40 45

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Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
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gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac 96
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
20 25 30

tgg tct gcc att tct aaa aat tac cca ttt gtt aac cga aca tct gtg 144
Trp Ser Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ser Val
35 40 45

atg att aag gat cgc tgg cgg acc atg aaa aag ctt ggc atg aac 189
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Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
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Met Ile Lys Asp Arg Trp Arg Thr Met Lys Lys Leu Gly Met Asn
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gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac 96
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
20 25 30

tgg tct gcc att tct aaa aat tac cca ttt gtt aac cga aca tct gtg 144
Trp Ser Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ser Val
35 40 45

atg att aag gat cgc tgg cgg acc atg aaa aga ctt ggc atg aac 189
Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn
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35 40 45

Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn
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Arg Arg Ala Ser Arg Ser Ser Gly Arg Ala Arg Arg Gly Arg His Glu
20 25 30

ccg ggg ctg ggg ggc ccg gcg gag cgc ggc gcg ggg gag gca cgg ctg 144
Pro Gly Leu Gly Gly Pro Ala Glu Arg Gly Ala Gly Glu Ala Arg Leu
35 40 45

gaa gag gca gtc aat cgc tgg gtg ctc aag ttc tac ttc cac gag gcg 192
Glu Ala Val Asn Arg Trp Val Leu Lys Phe Tyr His Glu Ala
50 55 60

ctg cgg gcc ttt cgg ggt agc cgg tac ggg gac ttc aga cag atc cgg 240
Leu Arg Ala Phe Arg Gly Ser Arg Tyr Gly Asp Phe Arg Gln Ile Arg
65 70 75 80

gac atc atg cag gct ttg ctt gtc agg ccc ttg ggg aag gag cac acc 288
Asp Ile Met Gln Ala Leu Leu Val Arg Pro Leu Gly Lys Glu His Thr
85 90 95

gtg tcc cga ttg ctg cgg gtt atg cag tgt ctg tgg cgg att gaa gaa 336
Val Ser Arg Leu Leu Arg Val Met Gln Cys Leu Ser Arg Ile Glu Glu
100 105 110

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Gly Glu Asn Leu Asp Cys Ser Phe Asp Met Glu Ala Glu Leu Thr Pro

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cag agt act gag ccc agc gca ggc ctc aac tcc tcc cag gag gcc gct Gln Ser Thr Glu Pro Ser Ala Gly Leu Asn Ser Ser Gln Glu Ala Ala 370	375	380	1152
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35 40 45

Glu Glu Ala Val Asn Arg Trp Val Leu Lys Phe Tyr Phe His Glu Ala
50 55 60

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Asp Ile Met Gln Ala Leu Leu Val Arg Pro Leu Gly Lys Glu His Thr
85 90 95

Val Ser Arg Leu Leu Arg Val Met Gln Cys Leu Ser Arg Ile Glu Glu
100 105 110

Gly Glu Asn Leu Asp Cys Ser Phe Asp Met Glu Ala Glu Leu Thr Pro
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130 135 140

Leu Thr Glu Ala Val Val Glu Ser Ser Arg Lys Leu Val Lys Glu Ala
145 150 155 160

Ala Val Ile Ile Cys Ile Lys Asn Lys Glu Phe Glu Lys Ala Ser Lys
165 170 175

Ile Leu Lys Lys His Met Ser Lys Asp Pro Thr Thr Gln Lys Leu Arg
180 185 190

Asn Asp Leu Leu Asn Ile Ile Arg Glu Lys Asn Leu Ala His Pro Val
195 200 205

Ile Gln Asn Phe Ser Tyr Glu Thr Phe Gln Gln Lys Met Leu Arg Phe
210 215 220

Leu Glu Ser His Leu Asp Asp Ala Glu Pro Tyr Leu Leu Thr Met Ala
225 230 235 240

Lys Lys Ala Leu Lys Ser Glu Ser Ala Ala Ser Ser Thr Gly Lys Glu
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Asp Lys Gln Pro Ala Pro Gly Pro Val Glu Lys Pro Pro Arg Glu Pro

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Tyr Gly Glu Gly Asn Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val			
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